

SEQUENCE LISTING

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<120> PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
 STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
 OF INHIBITORS THEREOF

<130> 0125-0049

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<223> full length mutant ERAB C214R

<400> 1

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<213> Homo sapiens

<223> full length mutant ERAB C214R

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Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu
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Val	Thr	Ser	Glu	Lys	Asp	Val	Gln	Thr	Ala	Leu	Ala	Leu	Ala	Lys	Gly
65					70					75					80

Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
100 105 110

Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
130 135 140

Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val
165 170 175

Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
195 200 205

Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
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Ile Arg Met Gln Pro
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 35 40 45
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 50 55 60
 Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
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 Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
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 Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
 100 105 110
 Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val
 115 120 125

Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
 130 135 140
 Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu
 145 150 155 160
 Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val
 165 170 175
 Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg
 180 185 190
 Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
 195 200 205
 Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro
 210 215 220
 Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
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 Ile Arg Met Gln Pro
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 aagtttggcc gtgtggatgt agctgtcaac tgtgcaggca tcgcgggtggc tagcaagacg 300
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<223> full length mutant ERAB C58V

<400> 6

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			20					25							
Gln	Gly	Ala	Ser	Ala	Val	Leu	Leu	Asp	Leu	Pro	Asn	Ser	C	Gly	Glu
		35					40					45			
Ala	Gln	Ala	Lys	Lys	Leu	Gly	Asn	Asn	Val	Val	Phe	Ala	I	Ala	Asp
	50					55					60				
Val	Thr	Ser	Glu	Lys	Asp	Val	Gln	Thr	Ala	Leu	Ala	Leu	I	Lys	Gly
	65				70					75				80	
Lys	Phe	Gly	Arg	Val	Asp	Val	Ala	Val	Asn	Cys	Ala	Gly	.	Ala	Val
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Ala	Ser	Lys	Thr	Tyr	Asn	Leu	Lys	Lys	Gly	Gln	Thr	His	C	Leu	Glu
			100					105							
Asp	Phe	Gln	Arg	Val	Leu	Asp	Val	Asn	Leu	Met	Gly	Thr	I	Asn	Val
		115					120					125			
Ile	Arg	Leu	Val	Ala	Gly	Glu	Met	Gly	Gln	Asn	Glu	Pro	I	Gln	Gly
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Gly	Gln	Arg	Gly	Val	Ile	Ile	Asn	Thr	Ala	Ser	Val	Ala	I	Phe	Glu
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Gly	Gln	Val	Gly	Gln	Ala	Ala	Tyr	Ser	Ala	Ser	Lys	Gly	C	Ile	Val
				165					170					175	
Gly	Met	Thr	Leu	Pro	Ile	Ala	Arg	Asp	Leu	Ala	Pro	Ile	C	Ile	Arg
			180					185							
Val	Met	Thr	Ile	Ala	Pro	Gly	Leu	Phe	Gly	Thr	Pro	Leu	I	Thr	Ser
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Leu	Pro	Glu	Lys	Val	Cys	Asn	Phe	Leu	Ala	Ser	Gln	Val	I	Phe	Pro
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Ser	Arg	Leu	Gly	Asp	Pro	Ala	Glu	Tyr	Ala	His	Leu	Val	C	Ala	Ile
	225				230					235				240	
Ile	Glu	Asn	Pro	Phe	Leu	Asn	Gly	Glu	Val	Ile	Arg	Leu	I	Gly	Ala
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gccccagccg acgtgacctc tgagaaggat gtgcaaacag ctctggctct agcaaaagga 240
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gtgcccttcc ctagccgact gggtgaccct gctgagtatg ctcacctcgt acaggccatc 720
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Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu
          35             40             45

Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp
          50             55             60

Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
          65             70             75             80

Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
          85             90             95

Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
          100            105            110

Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val
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Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
          130            135            140

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Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu
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Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val
165 170 175

Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg
180 185 190

Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
195 200 205

Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro
210 215 220

Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
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Ile Arg Met Gln Pro
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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<210> 10

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide for C58V

<400> 12
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<212> DNA
<213> Artificial Sequence

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35 40 45
Asn His Val Val Asp Glu Ile Gln Gln Leu Gly Gly Gln A Phe Ala
50 55 60
Cys Arg Cys Asp Ile Thr Ser Glu Gln Glu Leu Ser Ala L Ala Asp
65 70 75 80
Phe Ala Ile Ser Lys Leu Gly Lys Val Asp Ile Leu Val A Asn Ala
85 90 95
Gly Gly Gly Gly Pro Lys Pro Phe Asp Met Pro Met Ala A Phe Arg
100 105 1

Arg Ala Tyr Glu Leu Asn Val Phe Ser Phe Phe His Leu S Gln Leu
 115 120 125
 Val Ala Pro Glu Met Glu Lys Asn Gly Gly Gly Val Ile I Thr Ile
 130 135 140
 Thr Ser Met Ala Ala Glu Asn Lys Asn Ile Asn Met Thr S Tyr Ala
 145 150 155 160
 Ser Ser Lys Ala Ala Ala Ser His Leu Val Arg Asn Met A Phe Asp
 165 170 175
 Leu Gly Glu Lys Asn Ile Arg Val Asn Gly Ile Ala Pro C Ala Ile
 180 185 1
 Leu Thr Asp Ala Leu Lys Ser Val Ile Thr Pro Glu Ile C Gln Lys
 195 200 205
 Met Leu Gln His Thr Pro Ile Arg Arg Leu Gly Gln Pro C Asp Ile
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 Ala Asn Ala Ala Leu Phe Leu Cys Ser Pro Ala Ala Ser T Val Ser
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 Gly Gln Ile Leu Thr Val Ser Gly Gly Gly Val Gln Glu L Asn
 245 250 255

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 <213> Steptomyces hydrogenans

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 35 40 45
 Leu Gly Asp Ala Ala Arg Tyr Gln His Leu Asp Val Thr I Glu Glu
 50 55 60
 Asp Trp Gln Arg Val Val Ala Tyr Ala Arg Glu Glu Phe G Ser Val
 65 70 75 80
 Asp Gly Leu Val Asn Asn Ala Gly Ile Ser Thr Gly Met P Leu Glu
 85 90 95
 Thr Glu Ser Val Glu Arg Phe Arg Lys Val Val Glu Ile A Leu Thr
 100 105 1
 Gly Val Phe Ile Gly Met Lys Thr Val Ile Pro Ala Met L Asp Ala
 115 120 125

Gly Gly Gly Ser Ile Val Asn Ile Ser Ser Ala Ala Gly Leu Met Gly
130 135 140

Leu Ala Leu Thr Ser Ser Tyr Gly Ala Ser Lys Trp Gly Val Arg Gly
145 150 155 160

Leu Ser Lys Leu Ala Ala Val Glu Leu Gly Thr Asp Arg Ile Arg Val
165 170 175

Asn Ser Val His Pro Gly Met Thr Tyr Thr Pro Met Thr Ala Glu Thr
180 185 190

Gly Ile Arg Gln Gly Glu Gly Asn Tyr Pro Asn Thr Pro Met Gly Arg
195 200 205

Val Gly Glu Pro Gly Glu Ile Ala Gly Ala Val Val Lys Leu Leu Ser
210 215 220

Asp Thr Ser Ser Tyr Val Thr Gly Ala Glu Leu Ala Val Asp Gly Gly
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Trp Thr Thr Gly Pro Thr Val Lys Tyr Val Met Gly Gln
245 250

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<212> PRT

<213> Homo sapiens

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Tyr Ala Thr Leu Arg Asp Leu Lys Thr Gln Gly Arg Leu Trp Glu Ala
35 40 45

Ala Arg Ala Leu Ala Cys Pro Pro Gly Ser Leu Glu Thr Leu Gln Leu
50 55 60

Asp Val Arg Asp Ser Lys Ser Val Ala Ala Ala Arg Glu Arg Val Thr
65 70 75 80

Glu Gly Arg Val Asp Val Leu Val Cys Asn Ala Gly Leu Gly Leu Leu
85 90 95

Gly Pro Leu Glu Ala Leu Gly Glu Asp Ala Val Ala Ser Val Leu Asp
100 105 110

Val Asn Val Val Gly Thr Val Arg Met Leu Gln Ala Phe Leu Pro Asp
115 120 125

Met Lys Arg Arg Gly Ser Gly Arg Val Leu Val Thr Gly Ser Val Gly
130 135 140

Gly Leu Met Gly Leu Pro Phe Asn Asp Val Tyr Cys Ala Ser Lys Phe
145 150 155 160

Ala Leu Glu Gly Leu Cys Glu Ser Leu Ala Val Leu Leu Leu Pro Phe
165 170 175

Gly Val His Leu Ser Leu Ile Glu Cys Gly Pro Val His Thr Ala Phe
180 185 190

Met Glu Lys Val Leu Gly Ser Pro Glu Glu Val Leu Asp Arg Thr Asp
195 200 205

Ile His Thr Phe His Arg Phe Tyr Gln Tyr Leu Ala His Ser Lys Gln
210 215 220

Val Phe Arg Glu Ala Ala Gln Asn Pro Glu Glu Val Ala Glu Val Phe
225 230 235 240

Leu Thr Ala Leu Arg Ala Pro Lys Pro Thr Leu Arg Tyr Phe Thr Thr
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Glu Arg Phe Leu Pro Leu Leu Arg Met Arg Leu Asp Asp Pro Ser Gly
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Ser Asn

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<212> PRT

<213> Homo sapiens

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20 25 30

Gly Ala Thr Val Ala Ala Cys Asp Leu Asp Arg Ala Ala Ala Gln Glu
35 40 45

Thr Val Arg Leu Leu Gly Gly Pro Gly Ser Lys Glu Gly Pro Pro Arg
50 55 60

Gly Asn His Ala Ala Phe Gln Ala Asp Val Ser Glu Ala Arg Ala Ala
65 70 75 80

Arg Cys Leu Leu Glu Gln Val Gln Ala Cys Phe Ser Arg Pro Pro Ser
85 90 95

Val Val Val Ser Cys Ala Gly Ile Thr Gln Asp Glu Phe Leu Leu His
100 105 110

Met Ser Glu Asp Asp Trp Asp Lys Val Ile Ala Val Asn Leu Lys Gly
115 120 125

Thr Phe Leu Val Thr Gln Ala Ala Ala Gln Ala Leu Val Ser Asn Gly
 130 135 140
 Cys Arg Gly Ser Ile Ile Asn Ile Ser Ser Ile Val Gly Lys Val Gly
 145 150 155 160
 Asn Val Gly Gln Thr Asn Tyr Ala Ala Ser Lys Ala Gly Val Ile Gly
 165 170 175
 Leu Thr Gln Thr Ala Ala Arg Glu Leu Gly Arg His Gly Ile Arg Cys
 180 185 190
 Asn Ser Val Leu Pro Gly Phe Ile Ala Thr Pro Met Thr Gln Lys Val
 195 200 205
 Pro Gln Lys Val Val Asp Lys Ile Thr Glu Met Ile Pro Met Gly His
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 Leu Asp Glu Gln Phe Glu Pro Gln Lys Thr Leu Phe Ile Gln Cys Asp
 50 55 60
 Val Ala Asp Gln Gln Gln Leu Arg Asp Thr Phe Arg Lys Val Val Asp
 65 70 75 80
 His Phe Gly Arg Leu Asp Ile Leu Val Asn Asn Ala Gly Val Asn Asn
 85 90 95
 Glu Lys Asn Trp Glu Lys Thr Leu Gln Ile Asn Leu Val Ser Val Ile
 100 105 110
 Ser Gly Thr Tyr Leu Gly Leu Asp Tyr Met Ser Lys Gln Asn Gly Gly
 115 120 125

Glu Gly Gly Ile Ile Ile Asn Met Ser Ser Leu Ala Gly Leu Met Pro
 130 135 140
 Val Ala Gln Gln Pro Val Tyr Cys Ala Ser Lys His Gly Ile Val Gly
 145 150 155 160
 Phe Thr Arg Ser Ala Ala Leu Ala Ala Asn Leu Met Asn Ser Gly Val
 165 170 175
 Arg Leu Asn Ala Ile Cys Pro Gly Phe Val Asn Thr Ala Ile Leu Glu
 180 185 190
 Ser Ile Glu Lys Glu Glu Asn Met Gly Gln Tyr Ile Glu Tyr Lys Asp
 195 200 205
 His Ile Lys Asp Met Ile Lys Tyr Tyr Gly Ile Leu Asp Pro Pro Leu
 210 215 220
 Ile Ala Asn Gly Leu Ile Thr Leu Ile Glu Asp Asp Ala Leu Asn Gly
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 Asp Thr Thr Pro Phe Gln Ala Lys Thr Gln
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 20 25 30

Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu
 35 40 45

Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp
 50 55 60

Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
 65 70 75 80

Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
 85 90 95

Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
 100 105 110

Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val
 115 120 125

Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
 130 135 140

Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu
 145 150 155 160

Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val
 165 170 175

Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg
 180 185 190

Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
 195 200 205

Leu Pro Glu Lys Val Ala Asn Phe Leu Ala Ser Gln Val Pro Phe Pro
 210 215 220

Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
 225 230 235 240

Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala
 245 250 255

Ile Arg Met Gln Pro
 260

<210> 21

<211> 34

<212> DNA
 <213> Artificial Sequence

<220>
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 Oligonucleotide for C214A

<400> 21
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34

<210> 22
 <211> 786
 <212> DNA
 <213> Homo sapiens

<220>
 <223> full length mutant ERAB C214S

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 gacctgcca actcgggtgg ggaggcccaa gccaaagagt taggaaacaa ctgcgttttc 180
 gccccagccg acgtgacctc tgagaaggat gtgcaaacag ctctggctct agcaaaagga 240
 aagtttggcc gtgtggatgt agctgtcaac tgtgcaggca tcgcggtggc tagcaagacg 300
 tacaacttaa agaagggcca gaccatacc ttggaagact tccagcgagt tcttgatgtg 360
 aatctcatgg gcaccttcaa tgtgatccgc ctgggtggctg gtgagatggg ccagaatgaa 420
 ccagaccagg gaggccaacg tggggctatc atcaacactg ccagtgtggc tgccttcgag 480
 ggtcagggtt gacaagctgc atactctgct tccaaggggg gaatagtggg catgacactg 540
 cccattgctc gggatctggc tcccataggt atccgggtga tgaccattgc cccaggctcg 600
 tttggcacc cactgctgac cagcctccca gagaaagtgt ctaacttctt agccagccaa 660
 gtgccttcc ctagccgact gggtgaccct gctgagtatg ctcacctcgt acaggccatc 720
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 ccttaa 786

<210> 23
 <211> 261
 <212> PRT
 <213> Homo sapiens

<220>
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 Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Glu Arg Leu Val Gly
 20 25 30
 Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu
 35 40 45
 Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp
 50 55 60

Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
 65 70 75 80
 Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
 85 90 95
 Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
 100 105 110
 Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val
 115 120 125
 Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
 130 135 140
 Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu
 145 150 155 160
 Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val
 165 170 175
 Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg
 180 185 190
 Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
 195 200 205
 Leu Pro Glu Lys Val Ser Asn Phe Leu Ala Ser Gln Val Pro Phe Pro
 210 215 220
 Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
 225 230 235 240
 Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala
 245 250 255
 Ile Arg Met Gln Pro
 260

<210> 24

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 Oligonucleotide for C214S

<400> 24

ccagagaaag tgtctaactt cttagccagc caag